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- <110> Baker, Kevin P.  
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 tatgaaattg gccgatttca agaacacatc tccttttcaa ccccatctct 1150  
 tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200  
 agggagtccc accatcgctg gtggtatccc aggggtccctg ctcaagtttt 1250  
 ctttgaaaag gagggctgga atggtacatc acataggcaa gtcctgccct 1300  
 gtatttaggc tttgcctgct tgggtgtgatg taagggaat tgaaagactt 1350  
 gccattcaa aatgatcttt accgtggcct gcccctatgct tatgggtccc 1400  
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 aaaaaaaaa 1508

<210> 10  
 <211> 319  
 <212> PRT  
 <213> Homo sapiens  
  
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 <221> sig\_peptide  
 <222> 1-17  
 <223> Signal Peptide  
  
 <220>  
 <221> misc\_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212

<223> N-myristoylation Sites.

<220>

<221> misc\_feature

<222> 39-42

<223> Glycosaminoglycan Attachment Site.

<220>

<221> TRANSMEM

<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc\_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu
1				5					10					15

Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
				20					25					30

Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35					40					45

Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50					55					60

Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65					70					75

Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120

Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125					130					135

Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315

Pro Lys Ala Val

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 gcgggctggtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50  
 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggcggg 100  
 gcccttgagg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200  
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
 ggggttaaac cagcaaattc acccgtctta ccagctcctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650



gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
 agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800  
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
 gtgtccagggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
 ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000  
 aacctgtttg agagcacgat ccgcatacctg ggggggctcc tgagtgccta 1050  
 ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100  
 atcggctaata gcctgccttc agaacacat ccaagattcc ttactcggat 1150  
 gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200  
 cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
 cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
 caataccac agtggcctct tcacccacct gggcgtattc acgctgggcg 1400  
 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450  
 gggagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500  
 tgtcagaacg cacctgctgc ggcactccga gccagtaag ctcacctttg 1550  
 tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600  
 tgcttctctgc cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650  
 cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
 accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750  
 tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800  
 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850  
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900  
 ttcagccgat tcacacgggt ccctcgggt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
 tcttggggga gacgtcaag tatctgttct tgctcttctc cgatgacca 2050  
 aacctgtca gcctggacgc ctacgtgttc aacaccgaag cccacctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150  
 ggggtgggcag aggcaccttg ctgggtctgt ggcatTTTcc aaggGCCac 2200  
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250  
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 cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
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 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450  
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctcgtgaagc 2500  
 ctcatatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550  
 gcctgagggt ccagggtctg ctctgggtgt tacaagctgg actcagggat 2600  
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
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 ttgatttgct ctaaccgcaa 2720

<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
 1 5 10 15  
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
 20 25 30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro  
 35 40 45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
 50 55 60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
 65 70 75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
 80 85 90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe			

395				400				405						
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
				680					685					690

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtcct tcagtgaagt gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgctgc 50  
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tgttcgtct tccacctgtt cgtggcctgc ctctcgtgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
 cccaccgctt ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400  
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
 gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500  
 cagcgctcat caacgtgggc ttcctggaga gcagcaacag cacggactac 550  
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 ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700  
 cagcaactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggtgtggg 750  
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 ttttcgccc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850  
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
 acaggagcag ttcaaggtgg acaggaggagg aggcctgaac actgtgaagt 950  
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 ggccgccaag gcaggcttgg gctgggcccag gacacgtggg gtgcctggga 1250  
 cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300  
 cgggaccccc cctgccttcc tgctcacctt actctgacct ccttcacgtg 1350  
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450  
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM.  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
                   20                  25                  30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                   35                  40                  45  
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
                   50                  55                  60  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
                   65                  70                  75  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
                   80                  85                  90  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
                   95                  100                  105  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
                   110                  115                  120  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
                   125                  130                  135  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

	140		145		150
Glu Ser Ser Asn	Ser Thr Asp Tyr Ile	Ala Met His Asp Val	Asp		
	155	160	165		
Leu Leu Pro Leu	Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu	Ala		
	170	175	180		
Gly Pro Phe His	Val Ala Ser Pro Glu	Leu His Pro Leu Tyr	His		
	185	190	195		
Tyr Lys Thr Tyr	Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln	His		
	200	205	210		
Tyr Arg Leu Cys	Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp	Gly		
	215	220	225		
Arg Glu Asp Asp	Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu		
	230	235	240		
Gln Leu Phe Arg	Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr	Phe		
	245	250	255		
Arg His Leu His	Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys	Arg		
	260	265	270		
Ile Ala Ala Gln	Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu	Gly		
	275	280	285		
Gly Leu Asn Thr	Val Lys Tyr His Val	Ala Ser Arg Thr Ala	Leu		
	290	295	300		
Ser Val Gly Gly	Ala Pro Cys Thr Val	Leu Asn Ile Met Leu	Asp		
	305	310	315		
Cys Asp Lys Thr	Ala Thr Pro Trp Cys	Thr Phe Ser			
	320	325			

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
 gcgaacgctt cgaggagtcc tgg 23

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence



<222> 1-24  
 <223> Synthetic construct  
  
 <400> 19  
 gcagtgcggg aagccacatg gtac 24  
  
 <210> 20  
 <211> 46  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-46  
 <223> Synthetic construct.  
  
 <400> 20  
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46  
  
 <210> 21  
 <211> 494  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 21  
 caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
 aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
 gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
 gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200  
 tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250  
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 ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
 atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
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 taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494  
  
 <210> 22  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> sig\_peptide  
 <222> 1-15  
 <223> Signal peptide.  
  
 <220>  
 <221> misc\_feature  
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met	Leu	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Lys	Gly
1				5				10					15
Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser
			20					25					30
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro
			35					40					45
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Ser
			50					55					60
Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly	
			65					70					

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctggggccgc gccgcgctcc tgcccgcccg 150  
ggctccgggg cggcccgcta ggccagtgcg ccgccgctcg ccccgagggc 200  
cccggcccg cagcatggagc caccgggacg ccggcggggc cgcgcgcagc 250  
cgccgctgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300  
ggcgggcgcg gcgggcgcg cgcggcgctg cccgccggct gcaagcacga 350  
tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400  
tggtgtgcag cagcctggaa ctgcgcgagg tcctgcccgc agatactctg 450  
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500  
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550  
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600  
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 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000  
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050  
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 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950  
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 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500  
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 gtattctctg cggtttttta tctcacagta ctttatttct gtcttgtccc 2750  
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 ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850  
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<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu  
 1 5 10 15  
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
 20 25 30  
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
				95					100					105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	
				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
				125					130					135	
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
				140					145					150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
				155					160					165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
				170					175					180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
				185					190					195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
				200					205					210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
				215					220					225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	
				230					235					240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	
				245					250					255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
				260					265					270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
				275					280					285	
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	
				290					295					300	
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	
				305					310					315	
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	
				320					325					330	
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
				335					340					345	
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	
				350					355					360	
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
				365					370					375	
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	

	380		385		390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
	605	610	615		

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50

ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtctt ttgggagaac agattatatt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

tttggaagag tctgtctggg tgatcctggt agaagccca ttagggtcac 500

tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgac agtcggcatg 600  
 atgacgaagc cacgagaaca tcgacctcag aaggactgga ggaaggtgaa 650  
 gtggagggag agacgtcct gatcgtcgaa tcc 683

<210> 29  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-21  
 <223> Signal peptide.

<400> 29  
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu  
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 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
                   20                  25                  30  
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
                   35                  40                  45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
                   50                  55                  60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
                   65                  70                  75  
 Lys Gly Ser Gln Lys Ser  
                   80

<210> 30  
 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
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 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaacccg 150  
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200  
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250  
 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtcgt tggctagcgt 300  
 gggcgccctgg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350  
 tctgctttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
 caggcccgtc tccccctgtc ttggcgcaac ttccccatca ccttcgcctg 450



ctatgcggcc ctctttctgcc tctcggcctc catcatctac cccaccacct 500  
atgtccagtt cctgtcccac ggccgttcgc gggaccacgc catcgccgcc 550  
accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600  
gacccgggcc cggcccgccg agatcactgg ctatatggcc accgtacccg 650  
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ggcgggtgtac gccatctgct tcatacctagc ggccatcgcc atcctgctga 800  
acctggggga gtgcaccaac gtgctaccca tccccttccc cagcttcctg 850  
tcggggctgg ccttgtgtgc tgtcctcctc tatgccaccg cccttgttct 900  
ctggcccctc taccagttcg atgagaagta tggcggccag cctcggcgct 950  
cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg 1000  
gaccgcccac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050  
tgtggctgac ctggtgcact ctgccacct ggtttttgtc aaggtctaag 1100  
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gattctcact ctgtggcca ggctggagtg cagtgggtgc atctcagctc 1450  
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caagtagctg ggaggacagg tgtgagctgc cgcaccacgc ctgtttctct 1550  
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tcttatctgc ctgttttgca agcaccttct cctgtgtcct tgggagccct 1650  
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gtgtgtgtgt gtgtgtgttt ggggggtggg ggggtggtag ctggggattg 1850  
ggccctcttt ctcccagtgg aggaaggtgt gcagtgtact tcccctttaa 1900

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950  
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000  
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050  
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 cccaactatt ctctgtggta tgaaaaag 2128

<210> 31  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr  
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 Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg  
 20 25 30  
 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val  
 35 40 45  
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
 50 55 60  
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
 80 85 90  
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
 95 100 105  
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
 110 115 120  
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
 125 130 135  
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
 140 145 150  
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
 155 160 165  
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
 170 175 180  
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
 185 190 195  
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
				305					310					315	
His	Leu	Val	Phe	Val	Lys	Val									
				320											

<210> 32  
 <211> 3680  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 tttcaccatg ttggccaggc tgggtcttgaa ctcgtgacct catgatccgc 100  
 tcacctcggc ctcccaaagt gctgggatta caggcatgag ccactgacgc 150  
 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200  
 taaacattgg gcactacagt gaccaaaca gactgaattc cccaagagcc 250  
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
 ttattactca ctatgactaa gggtcacaaa tgggggtacgt tgatggagag 350  
 tgatttgta agagactaca gagggaggac agactaccaa gaggggggcc 400  
 aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450  
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 cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550  
 ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600  
 aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650  
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gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750  
 tgggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800  
 agaaggtgtg ggggttttgg ttccatcttg ccgagtctgc cggaatgtgg 850  
 atgggaagac caagaggagg agcaaggggc agaggggaag ggaatcttaa 900  
 agaagtccctg gatgccacac tcttcttcct tcctcctctt ccctctcctc 950  
 agaggtctca ctctgtggtt ttcatcttct gccctgcctc catctcctct 1000  
 ggggtgctggg aaagtggagg attagctgaa gttttgcttc tcggggcctg 1050  
 tctgaatctc cattgctttc tgggaggaca taattcacct gtcctagctt 1100  
 cttatcatct tacatttccc tgtagccact gggacatatg tgggtgttct 1150  
 tcctagctcc tgtctcctcc tcatgccttt gctgggtatg ggcatgttag 1200  
 ggggaaggtc attgctgtca gaggggcact gactttctaa tgggtgttacc 1250  
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 ccctaactat ccaggagatc gctgcgctgg ccaggtcctc cctgcatggt 1350  
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 gcacatccct ttggaactgt ttctgtgag tacatgctgg ggtctcccct 1450  
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 acatggatcc taactactgc cacccttcca cctccctgca cctgtgctcc 1550  
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 gccgagtggc tcacctcatt gagtggaagg gctggagcaa gccgagtgac 1700  
 tcacctgctg ccctggaatc agccttttcc tcctattcag acctcagcga 1750  
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 cccgccccca gccagggtgt taatgccac gtagtgagg cctctggcag 3450  
 atcctgcatt ccaaggtcac tggactgtac gtttttatgg ttgtgggaag 3500  
 ggtgggtggc tttagaatta agggccttgt aggctttggc aggtaagagg 3550  
 gcccaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600

ggctcattag gtgtttatatt tgttctatatt aagaatttgt tttattaaat 3650  
 taatataaaa atctttgtaa atctctaaaa 3680

<210> 33  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
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 Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser  
                   20                  25                  30  
 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val  
                   35                  40                  45  
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
                   50                  55                  60  
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
                   65                  70                  75  
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
                   80                  85                  90  
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
                   95                  100                 105  
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
                  110                 115                 120  
 Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
                  125                 130                 135  
 Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
                  140                 145                 150  
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp  
                  155                 160                 165  
 Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
                  170                 175                 180  
 Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
                  185                 190                 195  
 His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
                  200                 205                 210  
 Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
                  215                 220                 225  
 Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
                  230                 235                 240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
			335											

<210> 34  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct

<400> 34  
 tgtcctttgt ccagacttc tgtcc 25

<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 35  
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 37  
 ggcgagccct aactatccag gag 23

<210> 38  
 <211> 39  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-39  
 <223> Synthetic construct.

<400> 38  
 ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 39  
 ctgctgcaaa gcgagcctct tg 22

<210> 40  
 <211> 2084  
 <212> DNA  
 <213> Homo sapiens

<400> 40  
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 ccatctgttt tctctaagtc acgacagatt cctttcagac aggacaactg 150  
 tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200  
 tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250  
 caatctattc ttgccacatc aagggttgt tattccttta aaaaaaac 300



aataccaaag aagcctacaa tggtggcctt agccaaaatt ctgttgattt 350  
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaattctc aaggcgagtc attccccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650  
ccttgatcca tagctttggt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcccat ctacgcacat cccaatgcta cacctgctct 750  
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ccatctgtga ccccttgat agtggaacca agtggatggc ttaccacaaa 900  
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gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050  
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agaaatgaac cagttctgcg attagacaat gcaccggaac cttatgatgt 1200  
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250  
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cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350  
gcaagtgtca tctacatcct agccttttga caaattcctc tttcaaaagg 1400  
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450  
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aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650  
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catagcccag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900  
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000  
aagggttttg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
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Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagaagt ggaggccctc 150  
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300  
 tacaagtact tcatgccccaa gagcaccatt taccgtggag agatgtgctt 350  
 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400  
 tcttgctgtg gactgaggag gctgacattc gtgaggatga caacattgca 450  
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
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ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600  
 aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650  
 aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700  
 ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750  
 ttccgccttc gtgcgagaga cctcttgctg ggtttcaaca aacgtgccat 800  
 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggttaata 900  
 agaagtcaga gatttacaat atgactttta cattaagggtt tatgggatac 950  
 tcaagatatt tactcatgca tttactctat tgcttatgct ttaaaaaaag 1000  
 gaaaaaaaaaaa aaaactacta accactgcaa gctcttgtca aattttagtt 1050  
 taattggcat tgcttggttt ttgaaactga aattacatga gtttcatttt 1100  
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 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
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 tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300  
 tatcagatct caacattggt gggtttcttt gtttttcatt ttgtacaact 1350  
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 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
 tgtgtagggt ctgaatgctg taaggagttt aggttgatg aattctacaa 1550  
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30
Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45
Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu

50					55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
				65					70					75
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
				80					85					90
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
				95					100					105
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
				110					115					120
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
				125					130					135
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
				140					145					150
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
				155					160					165
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
				170					175					180
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
				185					190					195
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
				200					205					210
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
				215					220					225
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala
				230					235					240
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile
				245					250					255
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu							
				260										

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-20  
 <223> Synthetic construct.  
  
 <400> 45  
 gggaactgct atctgatgcc 20  
  
 <210> 46  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 46  
 caggatctcc tcttcagtc tgcagc 26  
  
 <210> 47  
 <211> 28  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-28  
 <223> Synthetic construct.  
  
 <400> 47  
 cttctcgaac cacataagtt tgaggcag 28  
  
 <210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 48  
 cacgattccc tccacagcaa ctggg 25  
  
 <210> 49  
 <211> 1969  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 49  
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ccgagcctcc cgccaccctg gaccccgcc ctcagcccca catcgatggg 350  
gccccagccc acaaccctgg ggggccatc acccccacc aacttcctgg 400  
atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450  
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agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600  
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ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750  
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<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

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Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	65	70	75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	80	85	90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	95	100	105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	110	115	120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	125	130	135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	140	145	150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	155	160	165	



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Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
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Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
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Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
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 <212> DNA  
 <213> Homo sapiens

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 <211> 440  
 <212> PRT  
 <213> Homo sapiens

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 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

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				80					85					90					
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala					
				95					100					105					
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val					
				110					115					120					
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val					
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Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile					
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Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro					
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				200					205					210					
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Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly
				380					385					390
Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser
				395					400					405
Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
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Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg
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 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

<400> 54

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
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Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
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Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
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				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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<212> DNA  
<213> Homo sapiens

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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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				20					25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57  
 <211> 4277  
 <212> DNA  
 <213> Homo sapiens

<400> 57

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<210> 58

<211> 1115

<212> PRT  
 <213> Homo sapiens

<400> 58

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Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu	275	280	285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met	290	295	300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr	305	310	315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser	320	325	330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu	335	340	345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala	350	355	360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala	365	370	375
Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	380	385	390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	395	400	405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	410	415	420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	425	430	435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	440	445	450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	455	460	465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	470	475	480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	485	490	495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	500	505	510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	515	520	525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	530	535	540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	545	550	555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg			

560										565					570				
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln					
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Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Ser	Gln	Pro	Asp				
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His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile					
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Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg					
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Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys					
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Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu					
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Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr					
				695					700					705					
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr					
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Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met					
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Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr					
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Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys					
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Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His					
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Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn					
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Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr					
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Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro					
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				845					850					855					



Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
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Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
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Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
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Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
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Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
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Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
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Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
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Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
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Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
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Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
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<223> Synthetic construct.

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<211> 24  
<212> DNA  
<213> Artificial

<220>  
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<400> 60  
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<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

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<210> 62  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
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cacgggcccgc gaggggtccc gcgcgctcag ccggcggtat ctgcccgcgc 150  
tgctgtcct gctactgtg ctgctgtgc ggcagcccg aaccgcgcgc 200  
gagaccacgc cgggcgcccc cagagccctc tccacgtgg gctccccag 250  
cctcttcacc acgcccgggtg tcccagcgc cctcactacc ccaggcctca 300  
ctacgccagg ccccccaaa accctggacc ttcggggtcg cgcgcaggcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400  
 cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
 tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
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 cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
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 cacatggaaa a 1661

<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63  
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 Tyr Leu Arg, Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg  
                   20                  25                  30  
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
                   35                  40                  45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
                   50                  55                  60  
 Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro  
                   65                  70                  75  
 Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser  
                   80                  85                  90  
 Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg  
                   95                  100                  105  
 Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe  
                   110                  115                  120  
 Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val  
                   125                  130                  135  
 Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp  
                   140                  145                  150  
 Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His  
                   155                  160                  165  
 Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala  
                   170                  175                  180  
 Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val  
                   185                  190                  195  
 Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser  
                   200                  205                  210  
 Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys  
                   215                  220                  225  
 Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met  
                   230                  235                  240  
 Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val  
                   245                  250                  255  
 Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala

260										265					270				
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro					
				275					280					285					
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu					
				290					295					300					
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly					
				305					310					315					
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu					
				320					325					330					
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg					
				335					340					345					
Ala	Val	Ile	Gly	Ser	Glu	Phe	Ile	Gly	Ile	Gly	Gly	Asn	Tyr	Asp					
				350					355					360					
Gly	Thr	Gly	Arg	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr					
				365					370					375					
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Xaa	Trp	Ser	Glu	Glu					
				380					385					390					
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg					
				395					400					405					
Gln	Val	Glu	Lys	Val	Arg	Glu	Glu	Ser	Arg	Ala	Gln	Ser	Pro	Val					
				410					415					420					
Glu	Ala	Glu	Phe	Pro	Tyr	Gly	Gln	Leu	Ser	Thr	Ser	Cys	His	Ser					
				425					430					435					
His	Leu	Val	Pro	Gln	Asn	Gly	His	Gln	Ala	Thr	His	Leu	Glu	Val					
				440					445					450					
Thr	Lys	Gln	Pro	Thr	Asn	Arg	Val	Pro	Trp	Arg	Ser	Ser	Asn	Ala					
				455					460					465					
Ser	Pro	Tyr	Leu	Val	Pro	Gly	Leu	Val	Ala	Ala	Ala	Thr	Ile	Pro					
				470					475					480					
Thr	Phe	Thr	Gln	Trp	Leu	Cys													
				485															

<210> 64  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 65  
 gtcacacaca gctctggcag ctgag 25

<210> 66  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 66  
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<210> 67  
 <211> 1564  
 <212> DNA  
 <213> Homo sapiens

<400> 67  
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 ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150  
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
 tccggtgcaa atgcatctgt ccacctata gaaacatcag tgggcacatt 250  
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
 gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
 agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
 atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450  
 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
 acaatgagga ggagaatgag gatgctcgt ctatggcagc agctgctgca 550  
 tccctcgggg gaccccagc aaacacagtc ctggagcgtg tggaagggtc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650  
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 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
 ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
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 ttttatttct ctca 1564

<210> 68  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
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 20 25 30  
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
 35 40 45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
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Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150  
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 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550  
 gcatgtgctg cccagtagcc cgctgcaata atggcatctg tatcccagtt 600  
 actgaaagca tcttaacccc tcacatcccc gctctggatg gtactcggca 650



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tcattttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
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 ctttattgcc aaagggttag ttctggtttt ctgcagccat tgcggttaa 2450  
 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
 accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550  
 aactcagttc taaatacttt gtctggagca caaaacaata aaagggttatc 2600  
 ttatagtcgt gactttaaac tttttagtag cacaattcac tttttagttt 2650  
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 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
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 caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850  
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 atataacaat tattatattt acaatttggg ttctgcaata tttttcttat 2950  
 gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000  
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 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
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 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25				30	

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40				45	

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	50	55	60
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	65	70	75
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	80	85	90
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	95	100	105
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	110	115	120
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	125	130	135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	140	145	150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	155	160	165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	170	175	180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	185	190	195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	200	205	210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	215	220	225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	230	235	240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	245	250	255

Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250  
atatttttagt aattcatatg ttttagatta taggttttaa cataacttg 300  
aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400  
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
ctcaagcccc caacatocca gtccctcagtc ctcagtcatc ttgacttcaa 600  
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
agcaccagag ccaggcagtc actgttcctc ctccctggtt ggagtccttt 700  
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800  
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
atacccccag cttctaagat cccagcttct gcagtggaaa tgcttggttc 900  
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ccagtagcaa tgtcttctc ttatgaccag agttctgtgc ataacaggat 1200  
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ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550  
tttaaagatg cttgggccag gcgggggtgg tgatgccat aatcccagtg 1600  
ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750  
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ctgaaaaga 1809

<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72  
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Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
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Leu Ile Arg

<210> 73

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-26

<223> Synthetic construct.

<400> 73

aattcatggc aaatatttcc cttccc 26

<210> 74

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 74

tggtaaactg gcccaaactc gg 22

<210> 75

<211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
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<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
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tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200  
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agaggccgcc tccacacccc tccccaggg gcttgggtggc agcatagccc 1250  
ccacccctgc ggcctttgct cacgggtggc cctgcccacc cctggcacia 1300  
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<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75



Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
				80					85					90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
				95					100					105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
				110					115					120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
				125					130					135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
				140					145					150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
				155					160					165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
				170					175					180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
				185					190					195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
				200					205					210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
				215					220					225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
				230					235					240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu
				245					250					255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu
				260					265					270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
				275					280					285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
				290					295					300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
				305					310					315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
				320					325					330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
				335					340					

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
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gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79  
<211> 475  
<212> PRT  
<213> Homo sapiens

<400> 79  
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser  
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala  
20 25 30  
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35 40 45  
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
50 55 60  
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
65 70 75  
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
80 85 90  
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395		400		405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser			
	410	415		420	
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu			
	425	430		435	
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly			
	440	445		450	
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser			
	455	460		465	
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile			
	470	475			

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 80  
 ttttgcggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			



	455	460	465
Lys Asp Asp Trp	Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala	Gly
	470	475	480
Glu His Thr Ala	Tyr Pro His Gly Trp	Val Glu Thr Ala Val	Lys
	485	490	495
Ser Ala Leu Arg	Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly	Pro
	500	505	510
Ala Ser Asp Thr	Ala Ser Pro Glu Gly	His Ala Ser Asp Met	Glu
	515	520	525
Gly Gln Gly His	Val His Gly Val Ala	Ser Ser Pro Ser His	Asp
	530	535	540
Leu Ala Lys Glu	Glu Gly Ser His Pro	Pro Val Gln Gly Gln	Leu
	545	550	555
Ser Leu Gln Asn	Thr Thr His Thr Arg	Thr Ser His	
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<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
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 ggagcacgga agggggtttc ccagaagaac aatgacctaa caagttgctg 450  
 cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500  
 tgtctgacaa tgggccctgc ttgggatata gaaaacaaa ccagccctac 550  
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600  
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aatttttgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000  
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agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150  
aggtaaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250  
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 aaaaactatt cttacatttg ttttgccttt cctcctattt ttttttaacc 2400  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			

	320		325		330
His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys	Val		
	335		340		345
Glu His Ala Tyr	Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser	Tyr		
	350		355		360
Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val	Val		
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
	380		385		390
Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys	Gly Ile Ile Arg His	Asp		
	440		445		450
Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
	455		460		465
Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
	470		475		480
Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
	485		490		495
Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
	530		535		540
Phe Thr Val Asn	Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr	Asn		
	545		550		555
Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
	560		565		570
Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		
	605		610		615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

<210> 87  
 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
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 ccaggacatt ggtgaccgcg caatccggta tggacgactg gaagcccagc 150  
 cccctcatca agcccttttg ggctcggaag aagcggagct ggtaccttac 200  
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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 35 40 45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
 50 55 60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105  
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
 110 115 120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
 125 130 135



Leu	Asn	Gln	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Asp	
				140					145					150	
Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn	
				155					160					165	
Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Cys	Thr	Val	Lys	Asp	Glu	
				170					175					180	
Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser	
				185					190					195	
Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp	
				200					205					210	
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His	
				215					220					225	
Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu	
				230					235					240	
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	
				245					250					255	
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser	
				260					265					270	
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr	
				275					280					285	
Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu	
				290					295					300	
Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn	Tyr	Leu	
				305					310					315	
Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro	
				320					325					330	
Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met	
				335					340					345	
Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro	
				350					355					360	
Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys	Ala	Ser	
				365					370					375	
Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe	Ala	Val	
				380					385					390	
Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	
				395					400					405	
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr	
				410					415					420	
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	

425										430					435				
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly					
				440					445					450					
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys					
				455					460					465					
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg					
				470					475					480					
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val					
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Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly					
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Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val					
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Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala					
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Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu					
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Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr					
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Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp					
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Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp					
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Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe					
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Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro					
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Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu					
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<222> 1-25

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Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
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Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	215	220	225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val				

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Tyr Val Ala Thr	Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly
	260	265	270
His Ser His Lys	Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg
	275	280	285
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	305		

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<212> DNA

<213> Homo sapiens

<400> 99

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<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile	365	370	375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu	380	385	390
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gctgcctgct ttgctagtgg gagccaacac cttgcctcc cacctcctct 2850  
ttgcagtagg ttgcccactg ctctgctctt ggccttctct gtgtgagagt 2900  
caagggtgct ggaagagaca gcagccccc ggaatgaag ctgatgccag 2950  
agtcagacct gaggaggaag aggagccact gatggagatg cggctccggg 3000  
atgcgcctca gcacttctat gcagcactgc tgcagctggg cctcaagtac 3050  
ctctttatcc ttggtattca gattctggcc tgtgccttg cagcctccat 3100  
ccttcgcagg catctcatgg tctggaaagt gtttgccctt aagttcatat 3150  
ttgaggctgt gggcttcatt gtgagcagcg tgggacttct cctgggcata 3200  
gctttggtga tgagagtga tgggtgctgt agctcctggc tcaggcagct 3250  
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acagagagtg ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350  
atctgcaaga caggctcagc catactctta ctatcatgca gccaggggcc 3400

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450  
 tgatccctaa ctctgattt ggatgcatct gagggacaag gggggcggtc 3500  
 tccgaagtgg aataaaatag gccgggctg gtgacttgca cctataatcc 3550  
 cagcactttg ggaggcagag gtgggaggat tgcttgggtcc caggagttca 3600  
 agaccagcct gtggaacata acaagacccc gtctctacta ttttaaaaaa 3650  
 agtgtaataa aatgataata t 3671

<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe
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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
				170					175					180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
				185					190					195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

200										205					210				
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp					
				215					220					225					
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys					
				230					235					240					
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met					
				245					250					255					
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr					
				260					265					270					
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp					
				275					280					285					
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu					
				290					295					300					
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro					
				305					310					315					
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu					
				320					325					330					
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala					
				335					340					345					
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala					
				350					355					360					
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser					
				365					370					375					
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala					
				380					385					390					
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala					
				395					400					405					
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr					
				410					415					420					
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala					
				425					430					435					
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg					
				440					445					450					
Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys					
				455					460					465					
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys					
				470					475					480					
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile					
				485					490					495					

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
	500	505	510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
	515	520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
	530	535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
	545	550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
	560	565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
	575	580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
	590	595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
	605	610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
	620	625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
	635	640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
	650	655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
	665	670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
	680	685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
	695	700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
	710	715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
	725	730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

785					790					795							
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly	800	805	810
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala	815	820	825
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu	830	835	840
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile	845	850	855
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu	860	865	870
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe	875	880	885
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr	890	895	900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile	905	910	915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser	920	925	930
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala	935	940	945
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp	950	955	960
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro	965	970	975
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu	980	985	990
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe	995	1000	1005
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu	1010	1015	1020
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg	1025	1030	1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe	1040	1045	1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly	1055	1060	1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe	1070	1075	1080



Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
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gcagttccct gtgtctctgg tggtttcct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgcct 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactcaa tctgaagtat aacgtgtctg tgttgaatac 350  
taaatacaac agaacgtggc cccagtgtgt gaccaaccac acgctggtgc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450  
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550  
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600  
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagcca gcgggaacct gaggcccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aatttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccagc aagagtcct 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
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ggcagtcctg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc 1200  
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggtgcg 1300  
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 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
 catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450  
 gccaacactt ccttttgcct tttgtttcct gtgcaaaca gtgagtcacc 1500  
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600  
 cgtgtgtgat tggttcatgc atgtaggctt cttaacaatg atgggtgggcc 1650  
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 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys  
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 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu  
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 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
 35 40 45  
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
 50 55 60  
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
 65 70 75  
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
 80 85 90  
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val  
 95 100 105  
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro  
 110 115 120  
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu  
 125 130 135  
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile  
 140 145 150  
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr  
 155 160 165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile		170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys		185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys		200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val		215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro		230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu		245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser		260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys		275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys		290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser		305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu		320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp		335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro		350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr		365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser		380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly		395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro		410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly		425	430	435
Leu	Tyr	Val	Gln	Met	Glu	Asn										440		

<210> 105

<211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-21  
 <223> Synthetic construct  
  
 <400> 105  
 cgctgctgct gttgctcctg g 21  
  
 <210> 106  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 106  
 cagtgtgccca ggactttg 18  
  
 <210> 107  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 107  
 agtcgcaggc agcggttg 18  
  
 <210> 108  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 108  
 ctctccgag tctgtgtgct cctgc 25  
  
 <210> 109  
 <211> 51  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

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c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cgccagcctg cgtctgccat ggggctcggg ttgaggggt ggggacgtcc 100

tctgtgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggccagatc atcgggggcc acgaggtgac cccccactcc 200

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ccccgactac caccatga ccacgcca cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcc 500

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ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600

ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650

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gggtttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750

ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800

ccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850

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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950

gccgtccag gcctggaatg ttccgtggct gggcccccac ggaagcctga 1000

tgttcaggg tggggtggga cgggcagcgg tggggcacac ccattccaca 1050

tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30

Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45

Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60

Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75

Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90

His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105

Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120

Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135

Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150

Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165

Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180

Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195

Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210

Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225

Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240

Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
275 280

<210> 112  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 112  
gacgtctgca acagctcctg gaag 24

<210> 113  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 113  
cgagaaggaa acgaggccgt gag 23

<210> 114  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 114  
tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115  
<211> 1808  
<212> DNA  
<213> Homo sapiens

<400> 115  
gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50  
cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggatcatcgtg acggggcgcca acacaggcat cgggaagcag accgccttgg 250  
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400  
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550  
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 ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650



gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700  
 tggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
 gctcattt 1808

<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
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 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
                   20                  25                  30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
                   35                  40                  45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
                   50                  55                  60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
                   65                  70                  75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
                   80                  85                  90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
                   95                  100                  105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
                   110                  115                  120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
                   125                  130                  135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
                   140                  145                  150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
                   155                  160                  165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
                   170                  175                  180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
                   185                  190                  195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
                   200                  205                  210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
                   215                  220                  225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	230	235	240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	245	250	255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	260	265	270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	275	280	285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	290	295	300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	305	310	315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	320	325	330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
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 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
 agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcatct actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggacctg agggagcagc aagggccctg atgcggctgc 450  
 aggacgtgta catgctcaat gtgaaaggcc tggcccaggg tgtctttcag 500  
 agagtcaact gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600  
 tgggggatta ttacatgcc attccatggc tggaggaggc tgtcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
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 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 cccaaccac gtggttagctg aggctgtcat ccagaggccc aatatacccc 900  
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000  
 ttccaacgcc tacctgctgc tccagcccct ccggaaggag gtcattccacc 1050  
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 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac caaaactgg tgaccctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450  
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500  
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550  
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 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
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 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800  
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 ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
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 cttgaccaca gggaccaaga agtggaatg aggacacctg caggaggggc 2050  
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100  
 agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala
1				5					10					15

Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
				20					25					30

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
				35					40					45

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55					60

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70					75

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85					90

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100					105

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115					120

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130					135

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145					150

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160					165

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175					180

Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly
				185					190					195

Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu
				200					205					210

Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser
				215					220					225

Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala
				230					235					240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

530

535

540

Ser Pro Glu Asp

&lt;210&gt; 119

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-23

&lt;223&gt; Synthetic construct.

&lt;400&gt; 119

cgggacagga gacccagaaa ggg 23

&lt;210&gt; 120

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-24

&lt;223&gt; Synthetic construct.

&lt;400&gt; 120

ggccaagtga tccaaggcat cttc 24

&lt;210&gt; 121

&lt;211&gt; 49

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-49

&lt;223&gt; Synthetic construct.

&lt;400&gt; 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

&lt;210&gt; 122

&lt;211&gt; 1778

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

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tcccaccctt aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
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 aagtgtctgtg gcggggagga ctaccgagat tggagcaaga atcagtagca 700  
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 gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
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 gcatcctcct gggcatcctg ctccccagc tcctgggggt gctgctgacg 950  
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 ggcagtgcct tggcgttgg attcaaggca gttttgtagc acctgtaatt 1450  
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 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

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 catgttttgt tttgttttta аааааааа 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe	1	5	10	15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly	170	175	180	
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn	185	190	195	
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val	200	205	210	
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile	215	220	225	
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly				



	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtggt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
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<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<400> 127

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tgcagttctc atcctcggcc caaaagtcat caaagaaaag ctgacacagg 200  
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agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350  
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450  
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<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480

Pro Val Ser Gln

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129

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ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
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 aaaaaaaaaa aaa 2213

<210> 130  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 50 55 60  
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
 65 70 75  
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
 80 85 90  
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp
				110					115					120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser
				125					130					135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg
				140					145					150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln
				155					160					165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val
				170					175					180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu
				185					190					195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met
				200					205					210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys
				215					220					225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg
				230					235					240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn
				245					250					255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His
				260					265					270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu
				275					280					285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys
				290					295					300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser
				305					310					315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr
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Ser	Phe	Leu	Met	Ser										
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 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

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 cttggcgctg gcggtactgg ccccgaggag aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctgggtcg tgagcgactc cttcgatgga 250  
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 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
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<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
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 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
 35 40 45  
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
 50 55 60  
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365										370					375				
Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Ser	Glu	Thr	Phe	Lys				
				380					385						390				
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser					
				395					400					405					
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg					
				410					415					420					
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile					
				425					430					435					
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr					
				440					445					450					
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln					
				455					460					465					
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val					
				470					475					480					
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile					
				485					490					495					
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln					
				500					505					510					
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln					
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Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val									
				530					535										

<210> 133  
 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
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 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
 catcaccag tgtgacatct atagaccct tctgggcctg cccgctgaca 350  
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctccctccctg 400  
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500  
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggata 550  
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
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 gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
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 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050  
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 ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250  
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300  
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<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
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                     20                    25                    30  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
                     35                    40                    45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50										55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala					
				65					70					75					
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile					
				80					85					90					
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr					
				95					100					105					
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala					
				110					115					120					
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro					
				125					130					135					
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro					
				140					145					150					
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile					
				170					175					180					
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr					
				185					190					195					
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg					
				200					205					210					
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser					
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Leu	Thr	Gly	Tyr	Val															
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<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
cgccatcgtg tccctgagcg agaccgcca atgtggtccc ccctgcacct 250
tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300
gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccactc 350

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 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
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 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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                     20                    25                    30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
                     35                    40                    45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
                     50                    55                    60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
                     65                    70                    75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
                     80                    85                    90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
                     95                    100                    105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
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<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctcagccccg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ctttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450  
 gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg agggccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
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 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys	1	5	10	15
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser	110													

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

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Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu				

	140		145		150
Ile Arg His His His Ser Glu His Arg	Val His Gly Ala Met Glu				
	155		160		165
Leu Gln Val Gln Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val Val				
	170		175		180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala Ala				
	185		190		195
Leu Ala Thr Gly Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro Leu				
	200		205		210
Ile Leu Leu Leu Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn Arg				
	215		220		225
Arg Ala Gln Glu Leu Val Arg Met Asp	Ser Asn Ile Gln Gly Ile				
	230		235		240
Glu Asn Pro Gly Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile Pro				
	245		250		255
Glu Ala Lys Val Arg His Pro Leu Ser	Tyr Val Ala Gln Arg Gln				
	260		265		270
Pro Ser Glu Ser Gly Arg His Leu Leu	Ser Glu Pro Ser Thr Pro				
	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu Asp				
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu	Val Ile				
	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc ctttctgcc ctcccttccct gccacccgct gcttctctggc 150  
 ccttctccga ccccgctcta gcagcagacc tcttgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250  
 ccgctcccggt accagcgcc tgaccctggg gaaaggatgg ttcccagagt 300  
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 actcccacgc tcgagcccg cagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcaccct tacttggagc cacaaggcct 450

gatgtactgc ctgctgctgta cctgctcaga gggcgcccat gtgagttggt 500  
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 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
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<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
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Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290										295					300				
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro					
				305					310					315					
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg					
				320					325					330					
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser					
				335					340					345					
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala					
				350					355					360					
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu					
				365					370					375					
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His					
				380					385					390					
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala					
				395					400					405					
Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro					
				410					415					420					
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala					
				425					430					435					
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys					
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Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gctcctcggt atcgtgaccc cgaggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgcctcc gtgggcgccg 400  
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtcgggaccg agataccatg ccaggactct ccgggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
                     20                    25                    30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
                     35                    40                    45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
                     50                    55                    60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
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 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
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 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 caggctgcca tggggcccag caccctctc ctcactttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgctctg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
tggaggccct gggaccaaag gcaaggaag aaggaatgag aagtacgata 500  
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600  
gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650  
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700  
gcttcccagag tccgggtgcc ctccccctgg gtaggcacag ggcagctggt 750  
atatggtggc tttcttttatt ttgctcggag gcctcctgga agacctggtg 800  
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
aaccgaacag tgggtggacag ctacgtattc ccagcagagg ggctgatccc 900  
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
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tcctttgatg ccagcggcac cctgaccctt gaacgggcag cactccctta 1200  
ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
catctttctc actcccatac atttatatta tatccccact aaatttcttg 1400  
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ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
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cccagacca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650  
agcagtgttc ttccctcag agtgacttgg ggagggagaa ataggaggag 1700  
acgtccagct ctgtcctctc ttccctcact ctcccttcag tgtcctgagg 1750  
aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 146

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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255



Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	260	265	270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	275	280	285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	290	295	300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	320	325	330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	335	340	345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	350	355	360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	365	370	375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	380	385	390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	395	400	405

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
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 gttctcctct tctctctaatt ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttctctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggg tccccggcc cacagcgaag tggaaaggct cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgctcatct gagccgagag gtggaatcca ggggtacagat 850  
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950  
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
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 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggagggtggc ggaggacaca ataaaagggt gcgctgtggg 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaatatc cggttttatc agcgtcttcc ccaggacccc acctacaaaa 1400  
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 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
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 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgttagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
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aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148  
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly  
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Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala  
20 25 30  
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
35 40 45  
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
50 55 60  
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
65 70 75  
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
80 85 90  
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
95 100 105  
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
110 115 120  
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
125 130 135  
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
140 145 150  
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
155 160 165  
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
170 175 180  
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
185 190 195  
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
200 205 210  
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
215 220 225  
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230					235					240				
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys
				245					250					255
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr
				395					400					405
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe
				410					415					420
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Thr	Cys	Arg
				425					430					435
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	Tyr	Asn
				440					445					450
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile	Cys	Pro	Val	Thr	Gln	Glu
				455					460					465
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg	Ala	Ser	Ala	Ile	Pro	Glu
				470					475					480
Thr	Ser	Asn	Ser	Glu	Ser	Ser	Ser	Gln	Ala	Thr	Thr	Pro	Phe	Leu
				485					490					495
Pro	Arg	Gly	Glu	Met										
				500										

<210> 149

<211> 24

<212> DNA  
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 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 149  
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 <210> 150  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.  
  
 <400> 150  
 ggaactgacc cagtgcctgac acc 23  
  
 <210> 151  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 151  
 gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45  
  
 <210> 152  
 <211> 2294  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 152  
 gcgatggtgc gcccggtggc ggtggcgggc gcggttgccg aggcttcctt 50  
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 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
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 cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
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 accgtccacc gacccttggc tgcgacttct ccagcccagt ccccgagagac 400

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gggtcataga ttacaaaat attttatata cttttattct cttactttat 1050  
atgttatatt taatgtcagg atttaaaac atctaattta ctgatttagt 1100  
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atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300  
taatcaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350  
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taccagtaca ttttgagac caaaagtaga ttaagcaggga attatcttta 1450  
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acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650  
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agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750  
taaatagagt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
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 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050  
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
 aactgctctg tgggtggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38



<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggaggcctc 150  
 ccgggaaaag ggctttgcc aaggagaagga catgaagaac gtcgtggggg 200  
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcc aatctctcac tcagctggag 400  
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600  
 gggctctgtg acctcgcca gtgtccaccc acctcgctca gcggctcccg 650  
 gggccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
     1                    5                    10                    15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
                     20                    25                    30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
                     35                    40                    45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
                     50                    55                    60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
                     65                    70                    75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
                     80                    85                    90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaaactgct gacgatgcag agttccgtga cgggtgcagga aggctgtgt 150
gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttacct 200
tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgccg gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctctt 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcg ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacacccctt atgatctcct ggataggag ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
 cgagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
 ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100  
 tggagccaca gccctggtct tctgtcctt ctgcgtcatc ttcgtttag 1150  
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250  
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttcacaga tggatgaagcc ttgggactcg cggggacagg aggcactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550  
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

110					115					120				
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu
				125					130					135
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile
				140					145					150
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser
				155					160					165
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp
				170					175					180
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser
				185					190					195
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser
				200					205					210
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn
				215					220					225
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr
				230					235					240
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly
				245					250					255
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu
				260					265					270
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu
				275					280					285
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser
				290					295					300
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala
				305					310					315
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln
				320					325					330
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val
				335					340					345
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe
				350					355					360
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys
				365					370					375
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu
				380					385					390
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr
				395					400					405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161

<211> 739

<212> DNA

<213> Homo sapiens

<400> 161

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gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
cctggaggag gaggatatca caggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
tgggggctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500
tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctacce tccagccatg acccttcct 650
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

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<210> 162

<211> 170

<212> PRT

<213> Homo sapiens

<400> 162

Met	Lys	Thr	Leu	Phe	Leu	Gly	Val	Thr	Leu	Gly	Leu	Ala	Ala	Ala
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Leu	Ser	Phe	Thr	Leu	Glu	Glu	Glu	Asp	Ile	Thr	Gly	Thr	Trp	Tyr

20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
			170											

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
cagggacctg gtacgtgaag gccatggtgg tcgataagga cttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169

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 cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150  
 gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200  
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250  
 cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300  
 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggagg 350  
 ctgtgagcag acccgagacg cactgagtc cttccccac cccggcttca 400  
 acaacagcct cccaacaaa gaccaccga atgacatcat gctggtgaag 450  
 atggcatcgc cagtctccat cacctgggt gtgcgacccc tcaccctctc 500  
 ctcacgtgt gtactgctg gcaccagctg cctcatttcc ggctggggca 550  
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 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
 gccaggtgta ctccgggggc cctctggtct gtaaccagtc ttttcaaggc 750  
 attatctcct ggggccagga tccgtgtgag atcacccgaa agcctggtgt 800  
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 acaattagac tggaccacc caccacagcc catcacctc catttccact 900  
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 aaaa 1204

<210> 170  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
 1 5 10 15



Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc gggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

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gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccgatgc tacattgatt ttgagattg aactttatgc 450  
 tgtgacaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
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 aaaaaaa 907

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 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
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 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu  
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 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn  
 35 40 45  
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr  
 50 55 60  
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg  
 65 70 75  
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly  
 80 85 90  
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro  
 95 100 105  
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly  
 110 115 120  
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu  
 125 130 135  
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser  
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

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<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>  
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<222> 1-18  
<223> Synthetic construct.

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-27  
<223> Synthetic construct.

<400> 185  
gcatcctgat atgacttgtc acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 186  
tacaagaggg aagaggagtt gcac 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-52  
<223> Synthetic construct.

<400> 187  
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cc 52

<210> 188  
<211> 573  
<212> DNA  
<213> Homo sapiens

<400> 188  
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cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150  
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 aacgccaggc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250  
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 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
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<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45

Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60

Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
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<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
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gactttggaa gtgaccacc atgggggtca gcatcttttt gtcctgtgtg 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
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cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
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ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500  
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
tgctcaacc tctccatcgt ctccatgcc acctgccatg gtgtgtatcc 650  
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caaggctctg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800



ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850  
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 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttgttg gcctgggaac ttcttggaac tttaactcct 1000  
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 tgaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194  
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 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg  
                     20                    25                    30  
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu  
                     35                    40                    45  
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala  
                     50                    55                    60  
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His  
                     65                    70                    75  
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly  
                     80                    85                    90  
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His  
                     95                    100                    105  
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
                     110                    115                    120  
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr  
                     125                    130                    135  
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His  
                     140                    145                    150  
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser  
                     155                    160                    165  
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile  
                     170                    175                    180  
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala  
                     185                    190                    195  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150  
 ggcttgctca aagccccgca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
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 caagaccac ctggagatga agaagatgat ctgagagggt acaggagggg 400  
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 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
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 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198  
<211> 1523  
<212> PRT  
<213> Homo sapiens

<400> 198  
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg  
1 5 10 15  
Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro  
20 25 30  
Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val  
35 40 45  
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro  
50 55 60  
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg  
65 70 75  
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu  
80 85 90  
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe  
95 100 105  
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys  
110 115 120  
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu  
125 130 135  
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg  
140 145 150  
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp  
155 160 165

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	170	175	180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Ile	Ser	Arg		185	190	195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	200	205	210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	215	220	225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	230	235	240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	245	250	255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	260	265	270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	275	280	285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	290	295	300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	305	310	315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	320	325	330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	335	340	345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	350	355	360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	365	370	375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	380	385	390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	395	400	405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	410	415	420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	425	430	435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	440	445	450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser			



455										460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser					
				470					475					480					
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe					
				485					490					495					
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg					
				500					505					510					
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg					
				515					520					525					
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn					
				530					535					540					
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys					
				545					550					555					
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys					
				560					565					570					
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu					
				575					580					585					
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val					
				590					595					600					
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn					
				605					610					615					
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser					
				620					625					630					
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr					
				635					640					645					
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu					
				650					655					660					
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly					
				665					670					675					
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys					
				680					685					690					
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala					
				695					700					705					
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln					
				710					715					720					
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val					
				725					730					735					
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met					
				740					745					750					

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr
	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile
	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe
	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg
	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser	Leu
	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro	Glu
	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly
	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu
	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser
	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr
	890	895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
	905	910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
	920	925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
	935	940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
	950	955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
	965	970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
	980	985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
	995	1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
	1010	1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
	1025	1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys

1040	1045	1050
Cys Ile Pro Leu Asp 1055	Lys Gly Phe Ser Cys 1060	Glu Cys Val Pro Gly 1065
Tyr Ser Gly Lys Leu 1070	Cys Glu Thr Asp Asn 1075	Asp Asp Cys Val Ala 1080
His Lys Cys Arg His 1085	Gly Ala Gln Cys Val 1090	Asp Thr Ile Asn Gly 1095
Tyr Thr Cys Thr Cys 1100	Pro Gln Gly Phe Ser 1105	Gly Pro Phe Cys Glu 1110
His Pro Pro Pro Met 1115	Val Leu Leu Gln Thr 1120	Ser Pro Cys Asp Gln 1125
Tyr Glu Cys Gln Asn 1130	Gly Ala Gln Cys Ile 1135	Val Val Gln Gln Glu 1140
Pro Thr Cys Arg Cys 1145	Pro Pro Gly Phe Ala 1150	Gly Pro Arg Cys Glu 1155
Lys Leu Ile Thr Val 1160	Asn Phe Val Gly Lys 1165	Asp Ser Tyr Val Glu 1170
Leu Ala Ser Ala Lys 1175	Val Arg Pro Gln Ala 1180	Asn Ile Ser Leu Gln 1185
Val Ala Thr Asp Lys 1190	Asp Asn Gly Ile Leu 1195	Leu Tyr Lys Gly Asp 1200
Asn Asp Pro Leu Ala 1205	Leu Glu Leu Tyr Gln 1210	Gly His Val Arg Leu 1215
Val Tyr Asp Ser Leu 1220	Ser Ser Pro Pro Thr 1225	Thr Val Tyr Ser Val 1230
Glu Thr Val Asn Asp 1235	Gly Gln Phe His Ser 1240	Val Glu Leu Val Thr 1245
Leu Asn Gln Thr Leu 1250	Asn Leu Val Val Asp 1255	Lys Gly Thr Pro Lys 1260
Ser Leu Gly Lys Leu 1265	Gln Lys Gln Pro Ala 1270	Val Gly Ile Asn Ser 1275
Pro Leu Tyr Leu Gly 1280	Gly Ile Pro Thr Ser 1285	Thr Gly Leu Ser Ala 1290
Leu Arg Gln Gly Thr 1295	Asp Arg Pro Leu Gly 1300	Gly Phe His Gly Cys 1305
Ile His Glu Val Arg 1310	Ile Asn Asn Glu Leu 1315	Gln Asp Phe Lys Ala 1320
Leu Pro Pro Gln Ser 1325	Leu Gly Val Ser Pro 1330	Gly Cys Lys Ser Cys 1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
 1340 1345 1350  
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
 1355 1360 1365  
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
 1370 1375 1380  
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
 1385 1390 1395  
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
 1400 1405 1410  
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
 1415 1420 1425  
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
 1430 1435 1440  
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
 1445 1450 1455  
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
 1460 1465 1470  
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
 1475 1480 1485  
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
 1490 1495 1500  
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
 1505 1510 1515  
 Glu Cys Gly Cys Leu Ala Cys Ser  
 1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gaggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct tttagattct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagcggcta caacaccaca gcccgcagcg tcctggatga cggcagcatc 350  
gactatggca tcttcagat caacagcttc gcgtgggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggttggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttctaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccg ttctcccaa tttccttct caaacttgga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
     1                    5                    10                    15  
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
                     20                    25                    30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
                     35                    40                    45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
                     50                    55                    60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
                     65                    70                    75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
                     80                    85                    90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
                     95                    100                    105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
                     110                    115                    120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
                     125                    130                    135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
                     140                    145

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
 ctcatgggct gcctgggtcac aggc 24

<210> 206  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 206  
 ccagtcggac aggtctctcc cctc 24

<210> 207  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 207  
 tcagtgaacca aggtgagca ggcg 24

<210> 208  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 208  
 ctacactcgt tgcaaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209  
 <211> 1648  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 caggccattt gcatccact gtccttgtgt tcggagccag gccacaccgt 50  
 cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100  
 tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
 gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
 gaggaatata ccacagggcat ggcagactgc atcttagtca acagccagtt 350  
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
 ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctcagttggt 450  
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550  
 ccctagtaca gctgctgga agattgacat cccaagattg ggagaggggt 600  
 catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgtga 650  
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
 atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctcctc 750  
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
 tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850  
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
 gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950  
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
 aaaaattttc ccctgaagca ttacagaaac agctctaccg atatgttacc 1050  
 aaactgctgg tataatcaga ttgtttttta gatctccatt aatgtcattt 1100  
 ttatggattg tagaccaggt ttgaaacca aaaaagaaac ctagaatcta 1150  
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300  
 tgtcattcca tggtcagcag agtattttaa ttatatatttc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450  
 ataattgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcactgtcat ctgttaggga atttttgttt gtccctgtctt tgcctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323



<212> PRT  
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val  
320

<210> 211  
<211> 1554  
<212> DNA  
<213> Homo sapiens

<400> 211  
gactacgccg atccgagacg tggctccctg ggccggcagaa ccatgttgga 50  
cttcgcgata ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc 100  
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250  
ccttctggtt tggcagggcg ctcgtggtta gtttgggcac tgttgatgta 300  
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
gttttgctat gaagtctggt acacagatgg taatgggttag tacatttgaa 600  
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
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 agcttggtatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
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<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	20	25	30	
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	35	40	45	
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	50	55	60	
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	65	70	75	
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	80	85	90	
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	95	100	105	
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	110	115	120	
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	125	130	135	
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu				

140					145					150				
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser
				155					160					165
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val
				170					175					180
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln
				185					190					195
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu
				200					205					210
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu
				215					220					225
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys
				230					235					240
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser
				245					250					255
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser
				260					265					270
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys
				275					280					285
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys
				290					295					300
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val
				305					310					315
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu
				320					325					330
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln
				335					340					345
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg
				350					355					360
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro
				365					370					375
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp
				380					385					390
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly
				395					400					405
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr
				410					415					420
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val
				425					430					435

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440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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tcagggtctg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150  
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300  
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
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tgggagtgca ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450  
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<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met	Gly	Arg	Val	Ser	Gly	Leu	Val	Pro	Ser	Arg	Phe	Leu	Thr	Leu
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Leu	Ala	His	Leu	Val	Val	Val	Ile	Thr	Leu	Phe	Trp	Ser	Arg	Asp
			20						25					30
Ser	Asn	Ile	Gln	Ala	Cys	Leu	Pro	Leu	Thr	Phe	Thr	Pro	Glu	Glu
				35					40					45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	50	55	60
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	65	70	75
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	80	85	90
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	95	100	105
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	110	115	120
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	125	130	135
Lys	Lys	Lys	Pro	Phe											140		

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
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 gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
 cgtgggctac aacttctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggctgcggt gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccgga tgtgcagcgt 550  
 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
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<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

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Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
          20          25          30

Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
          35          40          45

Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
          50          55          60

His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
          65          70          75

Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
          80          85          90

Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
          95          100          105

Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
          110          115          120

Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
          125          130          135

Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
          140          145          150

Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
          155          160          165

Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
          170          175          180

Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
          185          190          195

Pro
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<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150

cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcggaa 200
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 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350  
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 cccatctggg tgaccggggg caggccacag agggcaggcc agggctggaa 850  
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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
245 250

<210> 219  
<211> 2065  
<212> DNA  
<213> Homo sapiens

<400> 219  
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ccggggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400  
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gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
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 ttcaaataat ccataatctaa atttagtgca atatcttgct ttttgtatag 2000  
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<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
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Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
			20					25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35					40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
			50					55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	65	70	75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	80	85	90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	95	100	105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	110	115	120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	125	130	135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	140	145	150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	155	160	165
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	170	175	180
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	185	190	195
Phe	Leu	Val	Phe	Pro	Leu										200		

<210> 221  
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 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
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 <223> Synthetic construct.

<400> 221  
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<210> 222  
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 <212> DNA  
 <213> Artificial

<220>  
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 <223> Synthetic construct.

<400> 222  
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<210> 223  
 <211> 40

<212> DNA  
<213> Artificial

<220>  
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<222> 1-40  
<223> Synthetic construct.

<400> 223  
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<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150  
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
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<212> PRT

<213> Homo sapiens

<400> 225

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Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
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Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
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His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
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Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
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Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
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Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
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<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	320	325	330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	335	340	345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	350	355	360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	365	370	375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	380	385	390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	395	400	405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	410	415	420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	425	430	435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	440	445	450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	455	460	465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	470	475	480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	485	490	495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	500	505	510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	515	520	525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	530	535	540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	545	550	555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	560	565	570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	575	580	585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	590	595	600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly			



	605		610		615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp		
	620	625	630		
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu		
	635	640	645		
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His		
	650	655	660		
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser		
	665	670	675		
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val		
	680	685	690		
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr		
	695	700	705		
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile		
	710	715	720		
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val		
	725	730	735		
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg		
	740	745	750		
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val		
	755	760	765		
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile		
	770	775	780		
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp		
	785	790	795		
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
	800	805			

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 <213> Artificial

<220>  
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 <222> 1-50  
 <223> Synthetic construct.

<400> 230  
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<210> 231  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<221> Artificial Sequence  
<222> full  
<223> Synthetic oligonucleotide probe

<400> 231  
cctgagctgt aaccccactc cagg 24

<210> 232  
<211> 23  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 232  
agagtctgtc ccagctatct tgt 23

<210> 233  
<211> 2786  
<212> DNA  
<213> Homo sapiens

<400> 233  
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atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100  
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
acttgaagct caattttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250  
atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300  
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400  
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450  
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
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 tgttgttgtt ttgttttgtt ttttttgctt ttaccaaaca tgtctgtaa 2700  
 tcttaacctc ctgcctagga tttgtacagc atctggtgtg tgcttataag 2750  
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile	1	5	10	15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn	20	25	30	
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200  
aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250  
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300  
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350  
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aatcaccaaa ccatcaacag ggaccccagt cacaagccaa cacccattaa 1500  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20					25					30
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35					40					45
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50					55					60
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65					70					75
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80					85					90
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95					100					105
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110					115					120
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125					130					135
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140					145					150
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155					160					165
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170					175					180
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185					190					195
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

	200	205	210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe
	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

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<210> 238



<211> 47  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.  
  
 <400> 238  
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 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
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 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 239  
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 <213> Artificial  
  
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 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 240  
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 <210> 241  
 <211> 48  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.  
  
 <400> 241  
 ggcattctac ctttatggag tactctttgc tgttggcctc tgtgctcc 48  
  
 <210> 242  
 <211> 2436  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 242  
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 gaccacacgt cctggaagca ccagccttta tctcttcacc ttcaagtccc 150  
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200  
 ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250  
 aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc 300  
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 agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
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 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5					10					15
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	80	85	90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	95	100	105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala			

	365		370		375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala		
	380	385	390		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala		
	395	400	405		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala		
	410	415	420		
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala		
	425	430	435		
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val		
	440	445	450		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala		
	455	460	465		
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala		
	470	475	480		
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala		
	485	490	495		
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile		
	500	505	510		
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe		
	515	520	525		
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn		
	530	535	540		
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly		
	545	550	555		
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro		
	560	565	570		
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile		
	575	580	585		
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro			
	590	595			

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic sequence.

<400> 245  
 gtcagagttg gtggctgtgc tagc 24

<210> 246  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 246  
 ggaccagggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
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 ttcccgacct tccagcaat atgcatcttg cacgtctggt cggtcctgc 100  
 tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150  
 cccattgag aaggtcattg aagggatcaa ccgaggggtg agcaatgcag 200  
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
 tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaa 400  
 gaagcagaga agcttgggcca tggggtaaac aacgtgctg gacaggccgg 450  
 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
 ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550  
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tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
 tccagccatc aaggaggggc cacaaccacg ccgtagcct ctggggcctc 750  
 agtcaacacg cctttcatca accttccgc cctgtggagg agcgtcgcca 800  
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900  
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 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
 215 220 225  
 Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
 230 235 240  
 Ser Val Ala Asn Ile Met Pro  
 245

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 251  
 tgacccatt gagaaggat ttgaaggat caaccgagg ctg 43

<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens



<400> 252

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tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150  
ggggcgacc gcggggcgga gctgccgcc gtgagtccgg ccgagccacc 200  
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 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
1				5					10					15
Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

80					85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu Val Asn Arg	Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val			

	665		670		675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro		
	680	685	690		
Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys		
	695	700	705		
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val		
	710	715	720		
Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe		
	725	730	735		
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln		
	740	745	750		
Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu		
	755	760	765		
Pro Pro Glu Thr	Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr		
	770	775	780		
Pro Leu Asp His	Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro		
	785	790	795		
Gly Ala Arg Val	Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile		
	800	805	810		
Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg		
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Val Arg Leu Gly	Ser Glu Ile Arg Asp	Ser Val Val			
	830	835			

<210> 254  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 254  
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<210> 255  
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 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 255  
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<210> 256  
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<220>  
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 <223> Synthetic construct.

<400> 256  
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<210> 257  
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<400> 258  
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<210> 259  
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 <222> 3635  
 <223> unknown base

<400> 259  
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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	
				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530										535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu					
				545					550					555					
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu					
				560					565					570					
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu					
				575					580					585					
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
				590					595					600					
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
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Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
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Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
				665					670					675					
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
				680					685					690					
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
				695					700					705					
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
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Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725					730					735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740					745					750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755					760					765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
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Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
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<211> 24

<212> DNA  
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<220>  
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<222> 1-24  
<223> Synthetic construct.

<400> 261  
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<210> 262  
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<212> DNA  
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<220>  
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<222> 1-24  
<223> Synthetic construct.

<400> 262  
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<210> 263  
<211> 46  
<212> DNA  
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<220>  
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<400> 263  
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<210> 264  
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 aaaaatttta aacctacttg atattccata acaaagctga ttttaagcaaa 1250  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
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50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys					
				65					70					75					
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
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Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
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Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
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Leu Leu Lys Val Tyr  
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<210> 266  
<211> 2403  
<212> DNA  
<213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
				35					40					45
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu
				215					220					225
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu
				230					235					240
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile
				245					250					255
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

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<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

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 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
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 <211> 423  
 <212> PRT  
 <213> Homo sapiens

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 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
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 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
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 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala	35	40	45	
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75	



Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

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 <212> DNA  
 <213> Homo sapiens

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 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250  
 acgccctcaa tctgctcttt tgggttaatgt ccatcagtgt gttggcagtt 300  
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 aacgagggtg gaggaagcag tcattttgac ttactttcct gtggttcac 400  
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 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300  
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala	20	25	30	
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu	35	40	45	
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe	50	55	60	
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile	65	70	75	
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu	80	85	90	
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys	95	100	105	
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met	110	115	120	
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser				



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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
				20					25					30
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
				140					145					150
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
				185					190					195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
				260					265					270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
				305					310					315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
				320					325					330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335					340					345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350					355					360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365					370					375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380					385					390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
				395					400					405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
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Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu			
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<210> 276  
 <211> 3143  
 <212> DNA  
 <213> Homo sapiens

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 gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

290										295					300				
Phe	Asn	Val	Ile	Arg	His	Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro					
				305					310					315					
Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val					
				320					325					330					
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp					
				335					340					345					
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu					
				350					355					360					
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg					
				365					370					375					
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr					
				380					385					390					
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr					
				395					400					405					
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val					
				410					415					420					
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr					
				425					430					435					
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly					
				440					445					450					
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp					
				455					460					465					
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala					
				470					475					480					
Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala					
				485					490					495					
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg					
				500					505					510					
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu					
				515					520					525					
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg					
				530					535					540					
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser					
				545					550					555					
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala					
				560					565					570					
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala					
				575					580					585					

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggtga aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279  
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<210> 280  
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<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 280  
catcttgatca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
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ttccttctcc ctggggctct gctctcagag gctgccaaaa tctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagagg 250  
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450  
ggatatcatg gattccttaa agaagagaa cttcgacatg gtgatagttg 500  
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550  
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tggaactctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700  
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 catccagcat ggtgtgcccc tgggtgggat ccctctcttt ggagaccagc 1250  
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 ttaaagaagc tcaaggcaga gacattggct ctaaatga aacaaatcat 1350  
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 tctctcccca acctcactaa 2320

<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282  
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 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr  
                   20                  25                  30  
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile  
                   35                  40                  45  
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg  
                   50                  55                  60  
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln  
                   65                  70                  75  
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys  
                   80                  85                  90  
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly  
                   95                  100                  105  
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln  
                   110                  115                  120  
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys  
                   125                  130                  135  
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys  
                   140                  145                  150  
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile  
                   155                  160                  165  
 Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro  
                   170                  175                  180  
 Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met  
                   185                  190                  195  
 Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe  
                   200                  205                  210  
 Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile  
                   215                  220                  225  
 Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu  
                   230                  235                  240  
 Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe  
                   245                  250                  255  
 Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

260					265					270				
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
				290					295					300
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser
				440					445					450
Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr
				455					460					465
Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp
				470					475					480
His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu
				485					490					495
Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala
				500					505					510
Val	Trp	Trp	Leu	Arg	Gly	Ala	Arg	Lys	Val	Lys	Glu	Thr		
				515					520					

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial



<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 283  
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 <210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 284  
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 <210> 285  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 285  
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45  
  
 <210> 286  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 286  
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 gtgctgtccc atccagcagg gctaccctga agctctgggt gcagccctcc 200  
 cgtccagtgg gcaggcgggt tcatccctcc tttctctccc aaagcccaac 250  
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 caactagaga atgggtggta gtgagacact atagaattac taaggagaag 2250  
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170	175	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser			
	185	190	195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu			
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<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
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<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
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<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
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<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
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ttcccgcggg gccgtgactg ggcggggcttc agccatgaag accctcatag 200  
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<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 293  
 gctgacctgg ttcccatcta ctcc 24

<210> 294  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 294  
 cccacagaca cccatgacac ttcc 24

<210> 295  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

<400> 296  
gggcggcgagg atggggggccg ggggcggcg ggcgcgcact cgctgaggcc 50  
ccgacgcagg gccggggccg gccaggggcc gaggagcgcg gcggccagag 100  
cggggcccg gaggcgacgc cggggacgcc cgcgcgacga gcagggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
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caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350  
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400  
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
actggtcatg ctgctggagt ggtggtcctg cacggagtgt aactgttca 500  
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600  
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gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800  
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tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcatg 1150



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 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950  
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcttgacct 2000  
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050  
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100  
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 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850  
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900  
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gccccaacta 2950  
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000  
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050  
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50  
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100  
tgcttttagca ctggggcact tcttgcttat ttcttttgga ggaaaggggc 150  
tcagtttgtc ttgtgggggt ggtggcaggc aggcgggctt acgcctgata 200  
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250  
tagctgggggt ctgagacctg ctctctcagt aaaattcctg ggatctgcct 300  
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400  
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500  
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
ctggcctgac agaattctcat cttgtttaat gctctcataa gaccatttgt 650  
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
gttgatatgg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900  
 cggtgactgt gcttgatgaat tatctgggga tgcaggctct gattcagtag 950  
 gccaggttg ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgac 1100  
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150  
 tctgtactaa aaatacaca attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300  
 acagagtggag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile	1	5	10	15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe	20	25	30	
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly	35	40	45	
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val	50	55	60	
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp	65	70	75	
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr	80	85	90	
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln	95	100	105	
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu	110	115	120	
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr	125	130	135	
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu											

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
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 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400  
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 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750  
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 gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt 850  
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
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 ctccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150  
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tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
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 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450  
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500  
 gagggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600  
 aggcattggtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
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 aattatgggtt atttgtaa 1768

<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser  
 1 5 10 15  
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu  
 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro  
 65 70 75  
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala  
 80 85 90  
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly  
 95 100 105  
 Arg Arg Arg Asp

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305

gcgggcccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50  
 tgtcactgcc tcccgccgcc tccgtcccgc gccatgaccc agccggtgcc 100  
 ccggtctctc gtgcccgccg cgctggccct gggctcagcc gcaactggcg 150  
 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300  
 ggctgtgcag cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
 caggcccagc tcttgcccaa cctggcgcgg ctcatccagg ccaagaaggc 400  
 gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450  
 cgctgccgcg ggacggggcg gtggtgacct gcgaggtgga cgcgagccc 500  
 ccggagctgg gacggccctt gtggaggcag gccgaggcgg agcacaagat 550  
 cgacctccgg ctgaagcccg ccttgagac cctggacgag ctgctggcg 600  
 cgggcgaggg cggcacctc gacgtggccg tgggtgatgc ggacaaggag 650  
 aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg 700  
 catcctcgcc gtcctcagag tccgtggcg cggaaggtg ctgcaacctc 750  
 cgaaagggga cgtggcgccc gagtgtgtgc gaaacctaaa cgaacgcac 800  
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850  
 caccttgccc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30
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Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
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Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
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Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
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Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
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 <211> 2272  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
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<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
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Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
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Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
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Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

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Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
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Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
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Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
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				320					325					330					
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln					
				335					340					345					
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly					
				350					355					360					
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg					
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Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg					
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				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
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Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
				500					505					510	
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
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Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
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<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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				20					25					30
Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
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Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
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Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
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Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile



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Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
				230					235					240
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu
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Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
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Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
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Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
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Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335					340					345
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
				350					355					360
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His
				365					370					375

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

665										670					675				
Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu					
				680					685					690					
Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu					
				695					700					705					
Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu					
				710					715					720					
Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp					
				725					730					735					
His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp					
				740					745					750					
Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His					
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Arg	Asp	Leu	Asp	Glu	Leu	Pro	Arg	Ala	Val	Ala	Thr								
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 <213> Artificial

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<210> 312  
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 <213> Artificial

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 <223> Synthetic construct.

<400> 312  
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<210> 313  
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 <213> Artificial

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 <222> 1-45  
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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

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agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150  
ctcagcagtt tcagccagca gggactgac aggtgtgtgt cctggagtgg 200  
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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	
				20					25					30	
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	
				35					40					45	
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	
				50					55					60	
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	
				65					70					75	
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	
				80					85					90	
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	
				95					100					105	
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	
				110					115					120	
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	
				125					130					135	
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	
				140					145					150	
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
				155					160					165	
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
				170					175					180	
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
				185					190					195	
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
				200					205					210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
				215					220					225	
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
				230					235					240	
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	
				245					250					255	
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	
				260					265					270	
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	
				275					280					285	
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	
				290					295					300	
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro Gly	
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro	
335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys Ala	
350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
365	370	

<210> 316  
 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

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 gagtttgag aagccagacc cctgggcacc tctcccaagc ccaaggacta 250  
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aaggaaa 4407

<210> 317  
<211> 837  
<212> PRT  
<213> Homo sapiens

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Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu  
35 40 45  
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu  
50 55 60  
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75  
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90  
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105  
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120  
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135  
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

140	145	150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro Leu	
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His Ile	
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys Asn	
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg Ala	
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val Val	
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys Arg	
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys His	
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
				815					820					825
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cgggtgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

cagcagtggg ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50  
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgtttggtg tcctggccct aactctaatt gtcctgtttt 200  
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcaactgatg 350  
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
gaccatgtat tggatcaatc ccactctaata atcagtttct gagttacaag 650  
actttgagga ggaggagaa gatcttcaact ttcctgccaa cgaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750  
gaccgcgtcac gccagacaag caagtgagga agaacttcca ataaatgact 800  
atactgaaaa tggaatagaa tttgatccca tgctggaatga gagagggttat 850  
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900  
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000  
gggaggggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050  
atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100  
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
1				5					10					15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe
				80					85					90
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe
				95					100					105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys
				110					115					120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro
				125					130					135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe
				140					145					150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn
				155					160					165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn
				170					175					180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala
				200					205					210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro
				215					220					225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu
				230					235					240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe
				245					250					255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg
				260					265					270



Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly
				275					280					285
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys
				290					295					300
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly
				305					310					315

Arg Val

<210> 323  
 <211> 1174  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50  
 cagggaactg cccggctggc ctaggcaggc agccgcacca tggccagcac 100  
 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150  
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200  
 accaacaatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250  
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300  
 tggcgctgcc ccaagacctc caggctgccc gcgcctcat ggtcatctcc 350  
 tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
 cacgcgctgc gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450  
 gcggcacccct cttcctcctg gccggcctcc tgtgcatggt ggccgtctcc 500  
 tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgccag 550  
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600  
 cgtccctctc gctcattggt ggcaccctgc tttgctgtc ctgccaggac 650  
 gaggcaccct acaggcccta ccaggccccg cccagggcca ccacgaccac 700  
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750  
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800  
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850  
 gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900  
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950  
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100  
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150  
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 324  
 Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe  
 1 5 10 15  
 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp  
 20 25 30  
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser  
 35 40 45  
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly  
 50 55 60  
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu  
 80 85 90  
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu  
 110 115 120  
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala  
 125 130 135  
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro  
 140 145 150  
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr  
 155 160 165  
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu  
 170 175 180  
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln  
 185 190 195  
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala  
 200 205 210  
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val  
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
 gagctccoct caggagcgcg ttagcttcac accttcggca gcaggagggc 50  
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100  
 cacatgccaa gtgggtggcg tcctcctgtc catcctgggg ctggccggct 150  
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200  
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
 gacttccagc catgtcgcag gcagtgcgag ccctgatgat cgtaggcatc 350  
 gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400  
 ccgcatggc agcatggagg actctgcaa agccaacatg aactgacct 450  
 ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500  
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550  
 gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600  
 ttgggtgccc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650  
 gggggtgtga tgatgtgcat cgctgcccgg ggctggcac cagaagaaac 700  
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
 aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850  
 tccttccaag cagactatg tgtaatgctc taagacctct cagcacgggc 900  
 ggaagaaact ccgggagagc tcacccaaaa aacaaggaga tcccatctag 950  
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100  
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350  
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
 cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500  
 tcttattaca gcaacaccat tctaggagtt tctgagctc tccactggag 1550  
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600  
 atttttttta atttaagtc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcactttgg gaggtgagg aggaaggatc acttgagccc agaagttcga 1850  
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggtgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
 gtctaaaaaa ataaaaata aataatggaa cacagcaagt cctaggaagt 2100  
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

80					85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
			95						100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
			110						115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
			125						130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
			140						145					150
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
			155						160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
			170						175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
			185						190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
			200						205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
			215						220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
			230						235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
			245						250					255
Ser	Lys	His	Asp	Tyr	Val									
			260											

<210> 327  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50  
 gtagcagttc cggagtccag ctggctaaaa ctcattcccag aggataatgg 100  
 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150  
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200  
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250  
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300  
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggttt catgatggcc atccttggca 400  
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450  
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500  
 ccctgtgagc tgggttgcca atgcatcatc cagagatttc tataactcaa 550  
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600  
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgcgt 650  
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagtttgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850  
 caaagaaact ttgatttact gttcttaact gctaatctt aattacagga 900  
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaacccc aatgctttga ttgttctaga agtatagta atttgttttc 1000  
 taagggtggt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta 1150  
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaagggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
 atcctcttct ccagagggt ttttttttct tgtgtattaa attaacattt 1450  
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650  
 gagtacagac ttgagggttt catcaatata aataaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggtc tgtgaaaaat aaatttcctt cttgtacat ttctgttttag 1850  
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900  
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
 aatgaatgtg ttctatttgc ttatacatt tatattaata aattgtacat 2000  
 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328  
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly  
 1 5 10 15  
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp  
 20 25 30  
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn  
 35 40 45  
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile  
 50 55 60  
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met  
 80 85 90  
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu  
 110 115 120  
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile  
 125 130 135  
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn  
 140 145 150  
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu  
 155 160 165  
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
 170 175 180  
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr  
 185 190 195  
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His  
 200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val  
 215 220 225

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
 tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50  
 ctgggctggg tgaatggcct ggtctcctgt gccctgcca tgtggaaggt 100  
 gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150  
 gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300  
 ttgtctgggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
 cgcttggtgc tcacctctgg gattgtcttt gtcactctcag gggtcctgac 400  
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450  
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg gggtgctgtg 550  
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600  
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650  
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
 gagccatcca gaagtggcag tgcccaacag ctttgggatg gggtcgtacc 750  
 ttttgtttct gcctcctgct attttcttt tgactgagga tatttaaaat 800  
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850  
 gctgtttctc acccttggat gatggagcca aagaggggat gctttgagat 900  
 tctggatctt gacatgcca tcttagaagc cagtcaagct atggaactaa 950  
 tgcgagggct gcttgctgtg ctggccttgc aacaagacag actgtcccca 1000  
 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050  
 gctgcccccc atcctactca ggtctctgga gctcctctct tcacccttg 1100  
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccaggtcc 1200  
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250



gccccctcg tctcaccgcc ttacactca catttttatc aaataaagca 1360

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50  
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100  
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150  
gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtggg 200  
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250  
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300  
gcaagttcta tagctccttg ttggtctctc cgctgccct ggaaacagcc 350  
cgggccctca tgtgtgtggc tgttgcctc tccttgatcg cctgcttat 400  
tggcatctgt ggcataaagc aggtccagtg cacaggctct aacgagaggg 450  
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500  
atcttcgttc tgattccggt gagctggaca gccaataaa tcatcagaga 550  
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600  
cacttttctt tggctgggca agcgtgctg tcctcttcat tggagggggg 650  
ctgctttgtg gatatttctg ctgcaacaga aagaagcaag ggtacagata 700  
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750  
caatgcttag taagacctcc accagttagt tctaagcct ccttttggct 800  
ccaagtatgg actatggtca atgtttttta taaagtcctg ctagaaactg 850  
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900  
cgaaagtttc aatttgttac tggtggtagg aatgaaaatg acttacttgg 950  
acattctgac ttcagggtga ttaaagcat tgactattgt tggaccaat 1000  
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
caagtgtaca atgatggact acttattact ttttgacat catgtattat 1100  
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150  
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu	Leu Ala Leu Pro Pro	Ala Leu Glu Thr Ala	Arg
	20	25	30
Ala Leu Met Cys	Val Ala Val Ala Leu Ser	Leu Ile Ala Leu	Leu
	35	40	45
Ile Gly Ile Cys	Gly Met Lys Gln Val Gln	Cys Thr Gly Ser	Asn
	50	55	60
Glu Arg Ala Lys	Ala Tyr Leu Leu Gly Thr	Ser Gly Val Leu	Phe
	65	70	75
Ile Leu Thr Gly	Ile Phe Val Leu Ile Pro	Val Ser Trp Thr	Ala
	80	85	90
Asn Ile Ile Ile	Arg Asp Phe Tyr Asn Pro	Ala Ile His Ile	Gly
	95	100	105
Gln Lys Arg Glu	Leu Gly Ala Ala Leu Phe	Leu Gly Trp Ala	Ser
	110	115	120
Ala Ala Val Leu	Phe Ile Gly Gly Gly Leu	Leu Cys Gly Phe	Cys
	125	130	135
Cys Cys Asn Arg	Lys Lys Gln Gly Tyr Arg	Tyr Pro Val Pro	Gly
	140	145	150
Tyr Arg Val Pro	His Thr Asp Lys Arg Arg	Asn Thr Thr Met	Leu
	155	160	165
Ser Lys Thr Ser	Thr Ser Tyr Val		
	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50  
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100  
 ctcagaagct gctagtctgt ctcaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200  
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250  
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300  
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350  
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400  
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met	Lys	Ile	Thr	Gly	Gly	Leu	Leu	Leu	Leu	Cys	Thr	Val	Val	Tyr
1				5				10						15

Phe	Cys	Ser	Ser	Ser	Glu	Ala	Ala	Ser	Leu	Ser	Pro	Lys	Lys	Val
				20					25					30

Asp	Cys	Ser	Ile	Tyr	Lys	Lys	Tyr	Pro	Val	Val	Ala	Ile	Pro	Cys
				35					40					45

Pro	Ile	Thr	Tyr	Leu	Pro	Val	Cys	Gly	Ser	Asp	Tyr	Ile	Thr	Tyr
				50					55					60

Gly	Asn	Glu	Cys	His	Leu	Cys	Thr	Glu	Ser	Leu	Lys	Ser	Asn	Gly
				65					70					75

Arg	Val	Gln	Phe	Leu	His	Asp	Gly	Ser	Cys
				80					85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcg cccgcgcga tggctgcctc cccgcgcgg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaagtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaacat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgata tcctaattgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
gaagagttaa aacaacacat gtaaagcct tttgatattt catgggaatg 700  
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
1 5 10 15  
Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser  
20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50  
agccggggcg tcggtagcgc gccgggcaag gcaggcgcca tgaccctgat 100  
tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150  
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200  
gaccactgc ccagccgctc agggacccca acgcatccc agccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300  
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350  
 ggggtcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400  
 gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450  
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500  
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550  
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600  
 tgtccacgag agtcggtccc ccaaatcccc cctgcccgcc ggggtccgag 650  
 cccggccct cccggctgga aatcggcagc ctgctgctgc cctgctgct 700  
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
 ttccctgac cgcactctg ggccctggccg gcttcaccct gctcctcagt 800  
 ctcttgccct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850  
 agcgtcgccg gccctcccg accttgctcc ccgcgccgcg gcgggagctg 900  
 ctgcctgcc aggcccgct ctccggcctg cctcttcccg ctgccctgga 950  
 gccagccct gcgccgaga ggactcccg gactggcgga ggccccgcc 1000  
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050  
 cgactggga gtgggctcct cggggctcggg catctgctgt cgctgcctcg 1100  
 gccccgggca gagccgggcc gccccgggg cccgtcttag tgttctgccg 1150  
 gaggaccag ccgcctcaa tccctgacag ctcttgggc tgagttggg 1200  
 acgccaggtc ggtgggaggc tgggaaggg gagcggggag gggcagagga 1250  
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300  
 aaaaaaaaaa 1310

<210> 338  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens

<400> 338  
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe  
   1                  5                  10                  15  
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
                   20                  25                  30  
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
                   35                  40                  45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339  
 <211> 849  
 <212> DNA  
 <213> Homo sapiens

<400> 339  
 gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50  
 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100  
 caagacccta agaaccatca gccctcagct gcacctcctc cctccaagg 150  
 atgacaaagg cgctactcat ctatttggtc agcagcttctc ttgccctaaa 200  
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
 gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550  
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600  
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700  
 ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750  
 tcttggttc ctccttactc ccatctggac ccagtcccct gggttcctgtc 800  
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		



<210> 341  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.

<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 343  
atctcaggcg gcatacctgtc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24

<210> 345  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

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<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
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Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

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 <211> 23  
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<220>  
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 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
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<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
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<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
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<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcactct cccctcgaac ccaccagcc ccagcccgcc ccccggtgtg 200  
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 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
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                     20                    25                    30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
                     35                    40                    45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
                     50                    55                    60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
                     65                    70                    75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
                     80                    85                    90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
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 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
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Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150  
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 taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400  
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<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
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 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
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 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro  
155

&lt;210&gt; 357

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50  
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100  
ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150  
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250  
gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350  
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
tcagattcat ctctctga taatgaacaa ggcctccca gagtatgaag 550  
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
ctctttattc tgggtggacag tggatgaaa gaaaatggga aggtgatatc 650  
atctttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700  
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750  
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
aactcaaadc tcagagacac taaacaacag gatcactagg cctgccaacc 950  
acacacacac gcacgtgcac acacgcacgc acgctgcac acacacacgc 1000  
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100  
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
tcaaaaacca aaggatgggt ttaaaccact ttgtgaaatt gtctttttgc 1400  
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450  
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500  
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser  
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr  
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val  
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly  
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys  
260 265 270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagcaa 100  
cctcagcggg gaccgggct cagggacgcg gcggcggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggctcgt gctggcggcg gcgcttgggc 250  
tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900  
tccggcgga atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000



gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
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 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
 cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200  
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
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 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450  
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattggg 1500  
 ctatgccact tgaaaacaat ttgagaagt tttttgaagt ttttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 364  
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
   1                  5                  10                  15  
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
                   20                  25                  30  
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
                   35                  40                  45  
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
                   50                  55                  60  
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
                   65                  70                  75  
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
                   80                  85                  90  
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
                   95                  100                  105

Arg Ile Ser Trp	Ala Gly Asp Leu Asp	Lys Lys Asp Ala Ser	Ile
	110	115	120
Asn Ile Glu Asn	Met Gln Phe Ile His	Asn Gly Thr Tyr Ile	Cys
	125	130	135
Asp Val Lys Asn	Pro Pro Asp Ile Val	Val Gln Pro Gly His	Ile
	140	145	150
Arg Leu Tyr Val	Val Glu Lys Glu Asn	Leu Pro Val Phe Pro	Val
	155	160	165
Trp Val Val Val	Gly Ile Val Thr Ala	Val Val Leu Gly Leu	Thr
	170	175	180
Leu Leu Ile Ser	Met Ile Leu Ala Val	Leu Tyr Arg Arg Lys	Asn
	185	190	195
Ser Lys Arg Asp	Tyr Thr Gly Cys Ser	Thr Ser Glu Ser Leu	Ser
	200	205	210
Pro Val Lys Gln	Ala Pro Arg Lys Ser	Pro Ser Asp Thr Glu	Gly
	215	220	225
Leu Val Lys Ser	Leu Pro Ser Gly Ser	His Gln Gly Pro Val	Ile
	230	235	240
Tyr Ala Gln Leu	Asp His Ser Gly Gly	His His Ser Asp Lys	Ile
	245	250	255
Asn Lys Ser Glu	Ser Val Val Tyr Ala	Asp Ile Arg Lys Asn	
	260	265	

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50  
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100  
 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150  
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
 aggggcgcg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250  
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tgggtctccgc 300  
 agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350  
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400  
 agtggttgga gtttctgtag atggaaaaga agtctgggtca gaaggtttag 450  
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaaggT aatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val	350	355	360
Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg	365	370	

<210> 367

<211> 30  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-30  
<223> Synthetic construct.

<400> 367  
tggaagaa gtctggcag aaggttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggtt cattctcctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
aaaacctcag aacaactcat ttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
gtctaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac cgggtgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300  
 tcactgctct ggaaccagca ggatgttacc ttgtccctgt cacagcggca 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac cgggggccct ggatggcctg 450  
 gaagctggtg gctatgtctc ctctttgtc cctgcgtgct ccctggtgga 500  
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
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 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650  
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700  
 agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750  
 ttcgccaat actggatgta catcattccc gtcgtcctgt tctcatgat 800  
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
 agcttcagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250  
 ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300  
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350  
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
 ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
 cctcttctcc ctgacttact cactatgctg cttaacaaaa ctctctcaag 500  
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
 ctgctcttct cagccttcga ggctggtat atccatgagc acgtggaacg 600  
 gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
 tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
 gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750  
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 ctctgtcgg accgccgctg gctgctgctg ggcaccatac aagctctatt 900  
 tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950  
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
 tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100  
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 tccttcatag ctttctact tattgagttg gcttgtggat tatactttcc 1200  
 cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250  
 gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300  
 ctcttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
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 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
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 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650



ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
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Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Artificial

<400> 375  
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 gctccccgcg tgcgtcgcgg ccacaggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
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 ctctccaaga ctgggtggt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaccca ggcacagct gacatccccg cctcttcct gctcggccga 500  
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750  
 tttggcggtt gctaggctga aagggaagcc acaccactgg ccttccttc 800  
 cccaggcccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
 cccagggtct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcttgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccagggtt ctctgcacag tgaccttcac agcagttgtt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
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 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggatcaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcgactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val	1	5	10	15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys	20	25	30	
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly	35	40	45	
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr	50	55	60	
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys	65	70	75	
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile	80	85	90	
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe	95	100	105	
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu	110	115						

<210> 379  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 379  
 ctgcctccac tgctctgtgc tggg 24

<210> 380  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 380  
 cagagcagtg gatgttcccc tggg 24

<210> 381  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

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gccctgggat gcaccggcca gagggcatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgctc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttgga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
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ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650  
ggtatggggc catccgagct gagggcatct gtgtggtggt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
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Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20				25						30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35				40						45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca cccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250
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 ccattgtgat aaaaagagct cttaaagct gggaaataag tgggtgcttta 2100



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<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385  
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 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala  
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 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
 35 40 45  
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
 50 55 60  
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
 65 70 75  
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
 80 85 90  
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
 95 100 105  
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
 110 115 120  
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
 125 130 135  
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
 140 145 150  
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg  
 155 160 165  
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys  
 170 175 180  
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser  
 185 190 195  
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200										205					210				
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe					
				215					220					225					
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys					
				230					235					240					
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu					
				245					250					255					
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly					
				260					265					270					
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu					
				275					280					285					
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser					
				290					295					300					
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu					
				305					310					315					
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe					
				320					325					330					
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu					
				335					340					345					
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile					
				350					355					360					
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu					
				365					370					375					
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu					
				380					385					390					
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly					
				395					400					405					
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile					
				410					415					420					
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu					
				425					430					435					
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys					
				440					445					450					
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys					
				455					460					465					
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr					
				470					475					480					
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu					
				485					490					495					

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
500 505 510

Cys Glu Val

<210> 386  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 386  
ctgggatctg aacagtttcg gggc 24

<210> 387  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 387  
ggtccccagg acatggtctg tccc 24

<210> 388  
<211> 48  
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<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 388  
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
<211> 1449  
<212> DNA  
<213> Homo sapiens

<400> 389  
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100  
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tctgtctgct ggttttggtg 250  
 gcagctcttc tctgtggagc tgtggtcctc tgctccagc gctggctgag 300  
 gagaccccga attgattctc acaggcgac catggcagtt tttgctgttg 350  
 gagacttga ctctatttat gggacagaag cagctgtgag tccaactgtt 400  
 ggaattcacc ttcaaaactca aaccctgac ctatatcctg ttctgtctcc 450  
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500  
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
 tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaagaat 650  
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 attaagtctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
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 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
 tgtagataga aggtgaagga gattgctgaa gatataagagc acatataatg 1150  
 ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200  
 ctccatagtc catagtgttt ctctggagcc tcagggccttg gcatttattg 1250  
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
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 ctgacaaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr

1

5

10

15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 391  
 cttttcagtg tcacctcagc gatctc 26

<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-23  
 <223> Synthetic construct.

<400> 392  
 ccaaaacatg gagcaggaac agg 23

<210> 393  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 394  
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accaccggc gtttctccag ctcgatctgg aggtgcttc gccagtgtgg 100  
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt ttacaatct caagaaaaaa 450  
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gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600  
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tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750  
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cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850  
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900  
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aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser  
1 5 10 15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
                     20                    25                    30  
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
                     35                    40                    45  
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
                     50                    55                    60  
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
                     65                    70                    75  
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
                     80                    85                    90  
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
                     95                    100                    105  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
                     110                    115                    120  
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
                     125                    130                    135  
 Ser Gly Ser Ile Arg  
                     140

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
 cgcgccggg cgcgcggggt gagcgtgccg aggcggctgt ggcgcaggct 50  
 tccagccccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100  
 gggcccagac aaccgcggca tgcttccccg ggtgccaatg cgagggtggag 150  
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95					100					105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110					115					120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125					130					135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145					150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly Pro Thr Ile Leu	350		

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200  
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tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatatttaa 650  
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 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 402  
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 20 25 30  
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys  
 35 40 45  
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
 50 55 60  
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu  
 65 70 75  
 Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser  
 80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 403  
 ctctgtggt ctccagattt caggccta 28

<210> 404  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgtac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgtgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcccat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaattgaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650  
accacttatg atacagtga aactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttcttg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala		20	25	30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr		35	40	45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp		50	55	60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala		65	70	75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly		80	85	90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg		95	100	105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser		110	115	120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met		125	130	135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu		140	145	150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly		155	160	165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile		170	175	180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro		185	190	195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr		200	205	210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu		215	220	225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu		230	235	240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg		245	250	255
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr		260	265	270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly		275	280	285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met		290	295	300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg				



305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-31  
<223> Synthetic construct.

<400> 407  
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-34  
<223> Synthetic construct.

<400> 408  
gcggaattct taaaatggac tgactccact catc 34

<210> 409  
<211> 1487  
<212> DNA  
<213> Homo sapiens

<400> 409  
cgacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50  
tcttgcgcgc ggcctgaag tcggcgtggg cgtttgagga agctgggata 100  
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150  
tagataattt tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200  
agaaatgctg tggcatctgt tgcgcagggt atattgtttt ttacaggctg 250  
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300  
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350  
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450  
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggtgcatat 500  
gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700  
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
 ttgaaatagt tttatgaaat ttctttatatt ttcattgcat agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
 tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900  
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950  
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000  
 ttgaggtaaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100  
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
 aggttgagct gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200  
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaagggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggtg aagaaaaaat atttggttctt atgtattgaa gaagtgtact 1400  
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450  
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1				5					10					15
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
				155										

<210> 411  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 411  
 gtttgaggaa gctgggatac 20

<210> 412  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 412  
 ccaaactcga gcacctgttc 20

<210> 413  
 <211> 40  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-40  
 <223> Synthetic construct.

<400> 413  
 atggcaggct tctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100  
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtgggtggc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350  
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450  
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgccagcc 500  
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550  
tactatgtgc tttgaagacc gcatgatcat gagtctgtg aaaaacaatg 600  
tgggcagagg cctaaacatc gccctgggtga atggaaccac gggagctgtg 650  
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700  
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750  
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800  
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850  
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900  
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
gagatggagg gctgcatgcc cccgaagcca ttttaggtg gctgtggctc 1000  
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050  
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100  
gcaggtcctt gcacgtgtg tcggcctct cctcctcgga aacagaacct 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atgggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaa aaaaaaa 1337

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala  
   1                  5                  10                  15  
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
                   20                  25                  30  
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
                   35                  40                  45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
                   50                  55                  60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
                   65                  70                  75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
                   80                  85                  90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
                   95                  100                  105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
                   110                  115                  120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
                   125                  130                  135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
                   140                  145                  150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
                   155                  160                  165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
                   170                  175                  180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
                   185                  190                  195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
                   200                  205                  210  
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
                   215                  220

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-21  
 <223> Synthetic construct.  
  
 <400> 416  
 gccatagtca cgacatggat g 21  
  
 <210> 417  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 417  
 ggatggccag agctgctg 18  
  
 <210> 418  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
 aaagtacaag tgtggcctca tcaagc 26  
  
 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
 tctgactcct aagtcaggca ggag 24  
  
 <210> 420  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
 atttctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tgggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200  
ctctctctct gcctgtccta gtctcttagt cctcaaattc ccagtcccct 250  
gcaccccttc ctgggacact atgttggttct ccgccctcct gctggagggtg 300  
atgttgatcc tggetgcaga tgggggtcaa cactggacgt atgagggccc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900  
 cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050  
 cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100  
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
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 ggggtgtaga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
 ccttccccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450  
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
 gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550  
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
 tttccctaga tatactgagg gatctctcct taggataaag agttgctgtt 1650  
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
 t 1701

<210> 423  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 423  
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
 1 5 10 15  
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
 20 25 30  
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
 35 40 45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
 50 55 60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
 65 70 75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu



80					85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala
				95										105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly
				110										120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His
				125										135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala
				140										150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu
				155										165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His
				170										180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro
				185										195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe
				200										210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val
				215										225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln
				230										240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro
				245										255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn
				260										270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr
				275										285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly
				290										300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile
				305										315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser
				320										330
Ala	Gln	Ala	Thr	Thr	Glu	Ala								
				335										

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 424  
 gtaaagtcgc tggccagc 18  
  
 <210> 425  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 425  
 cccgatctgc ctgctgta 18  
  
 <210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 426  
 ctgcactgta tggccattat tgtg 24  
  
 <210> 427  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 427  
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45  
  
 <210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 428  
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
  
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaadc 300  
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350  
 gggttgaatg tacaacagca actgcacca catgtgttac caattttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcatc atccattcct tgttcccgga aggcattctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagtgcct 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgtgcctt ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg  
 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210> 430  
 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

<400> 430  
 ggagagagggc ggcgagggtga aaggcgcatt gatgcagcct gcggcggcct 50  
 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100  
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150  
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200  
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250  
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350  
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600  
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700  
 aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750  
 gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
 tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
 ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
 tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
 aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc 1100  
 acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
 aatttgtaaa tgttaagaat tttttttata tctgttaaata aaaaattatt 1250  
 tccaaca 1257

<210> 431  
 <211> 243  
 <212> PRT  
 <213> Homo Sapien

<400> 431  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
 1 5 10 15  
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
 20 25 30  
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial Sequence

<400> 432  
 aggacttgcc ctcaggaa 18

<210> 433  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 cgcaggacag ttgtgaaaat a 21

<210> 434  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 435  
 cccacctgta ccaccatgt 19  
  
 <210> 436  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 436  
 actccaggca ccattctgttc tccc 24  
  
 <210> 437  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 437  
 aagggtctggc attcaagtc 19  
  
 <210> 438  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 438  
 tgacctggca aaggaagaa 19  
  
 <210> 439  
 <211> 21  
 <212> DNA  
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 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 439  
 cagccaccct ccagtccaag g 21  
  
 <210> 440  
 <211> 19  
 <212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtgtt ttggagaga 19

<210> 441  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gagcaccaat 20

<210> 442  
<211> 25  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttaaagttcc aaga 24

<210> 444  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe



<400> 445  
 agcgtacact ctctccaggc aaccag 26  
  
 <210> 446  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 446  
 caattctgga tgagggtgga ga 22  
  
 <210> 447  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 447  
 caggactgag cgcttggtta 20  
  
 <210> 448  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 448  
 caaagcgcca agtaccggac c 21  
  
 <210> 449  
 <211> 18  
 <212> DNA  
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 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 449  
 ccagacctca gccaggaa 18  
  
 <210> 450  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 450  
 ccctagctga ccccttca 18

<210> 451  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 451  
tctgacaagc agttttctga atc 23  
  
<210> 452  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 452  
ctctccccct cccttttctt ttgttt 26  
  
<210> 453  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 453  
ctctggtgcc cacagtga 18  
  
<210> 454  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 454  
ccatgcctgc tcagccaaga a 21  
  
<210> 455  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 455  
caggaaatct ggaaacctac agt 23  
  
<210> 456  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gacccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461  
tggacacgtg gcagtgga 18

<210> 462  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
tcatggtctc gtcccattc 19

<210> 463  
<211> 27  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 463  
caccatttgt ttctctgtct ccccatc 27

<210> 464  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 464  
ccggcatcct tggagtag 18

<210> 465  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 465  
tccccattag cacaggagta 20

<210> 466  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 472  
tcagggtcta catcagcctc ctgc 24

<210> 473  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
aaggccaagg tgagtccat 19

<210> 474  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
cctactgagg agccctatgc 20

<210> 475  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
tccaggtgga cccacttca gg 22

<210> 476  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 476  
gggaggctta taggcccaat ctgg 24

<210> 477  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50